

Applicant: Rajasekhar Bandaru

Title: 6873 and 69112, Protein Kinase Molecules and Uses Therefor

USIN: 10/024,036

Filed: December 17, 2001

Attorney/Agent: Jean M. Silveri

Docket No.: MPI2000-521PIRM

Sheet 1 of 8 Sheets

10074036.070502

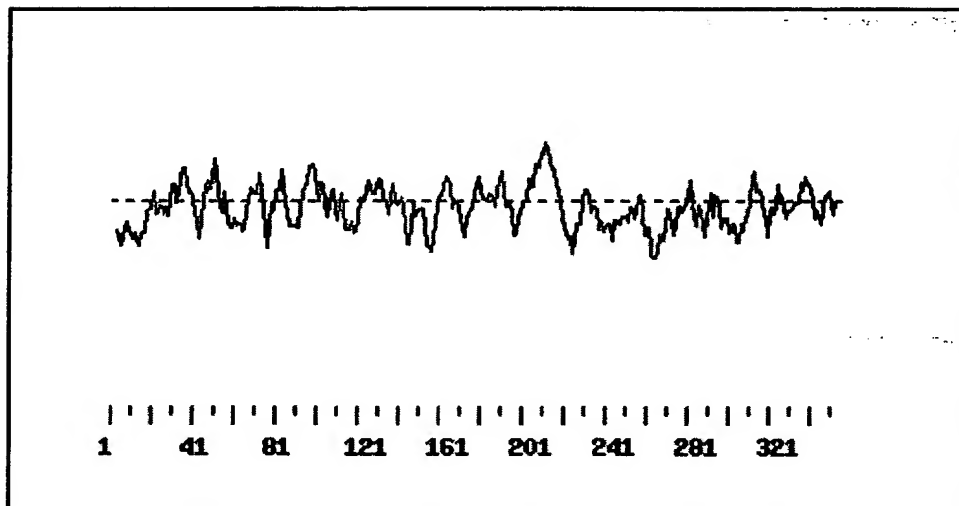


FIGURE 1

Applicant: Rajasekhar Bandaru

Title: 68730 and 68731 Protein Kinase Molecules and Uses Therefor

USPN: 10/000,036

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Sheet 2 of 8 Sheets

10024036.070502

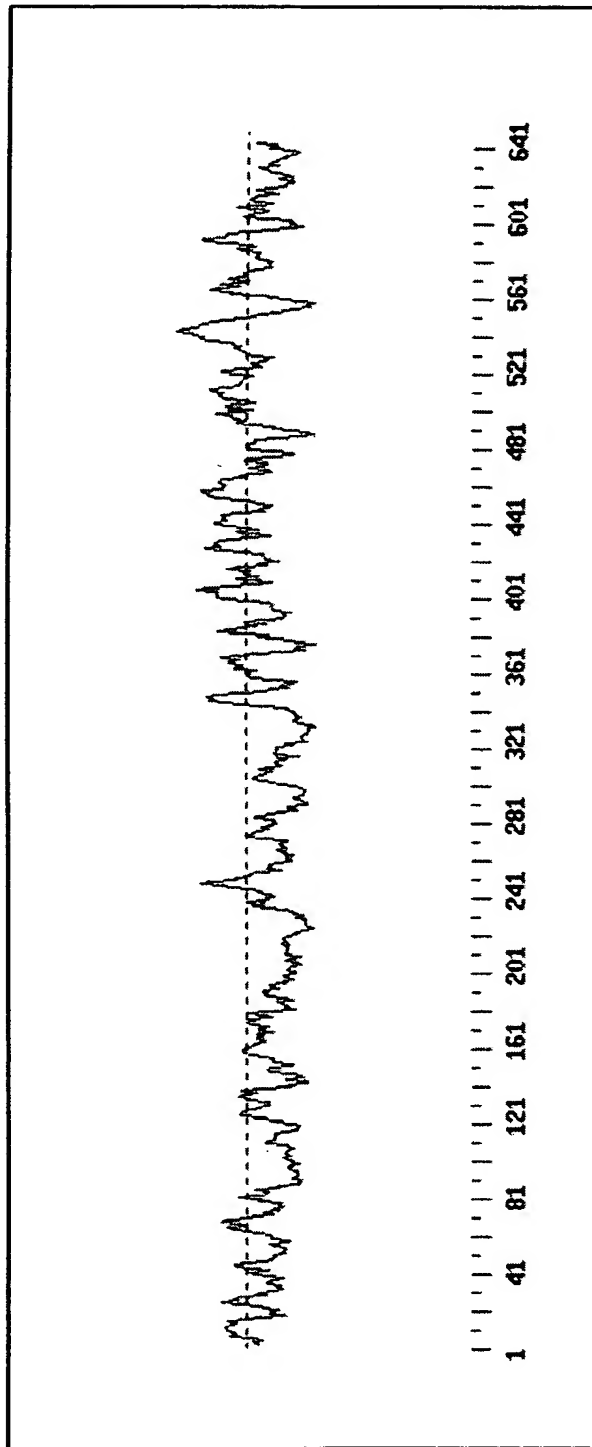


FIGURE 2

Applicant: Rajasekhar Bandaru

Title: 68730 69112, Protein Kinase Molecules and Uses

Therefor

US\$1: 10/024,036

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pkinese: domain 1 of 1, from 23 to 279: score 346.3, E = 3.4e-100
*->yelleklGeGsfgkVykakhk.tgkivAvKilkkesls.....lrE
+e++e+lG G+f++V +a++k tgk++AvK+++k+ l+++++ +E
68730 23 FEFKETLGTGAFSEVVLAEEKaTGKLFVAVKCIPKKALKgkessiENE 69
↑ ↑
iqilkrIsHpNIvrllgvfedtdhhlylvmEymegGdLfdylrrngplse
i++l++++H+Niv l +++e +++hlylvm+++ gG+Lfd++++g ++e
68730 70 IAVLRKIKHENIVALEDIYE-SPNHLYLVMQLVSGGELFDRIVEKGFYTE 118
↑ ↑
keakkialQilrGleYlHsngivHRDLKpeNILlden...gtvKiaDFGL
k+a +++Q+l ++ YLH++givHRDLKpeN+L +++++ t+ i+DFGL
68730 119 KDASTLIRQVLDAVYYLHRMGIVHRDLKPENLLYYSQdeeSKIMISDFGL 168
↑ ↑ ↑ ↑
Arll...eklthfvGTpwYmmAPEvilegrgysskvDvWSlGviLyEllt
++ +++ +++t +GTp+Y+ APEv l +++ys++vD WS+Gvi y ll+
68730 169 SKMEgkgDVMSTACGTPGYV-APEV-LAQKPYSKAVDCWSIGVIAYILLC 216
ggplfpgadlpafthggdevdqliifvlklPfsdelpktridpleelfrik
g +Pf+d ++ ++lf+ +
68730 217 G-----YPPFYD-----ENDSKLFEQI 233
kr.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<
++ + + +p ++ +S+++kd+++ + +kDP+kR+ t++++ hpw+
68730 234 LKaeyefDSPYWDDISDSAKDFIRNLMEKDPNKRY---TCEQAARHPWI 279

-*

FIGURE 3A

serkin_6: domain 1 of 1, from 23 to 279: score 386.6, E = 2.5e-112
 *->YellkklGkGaFGkVylardkktgrlvAiKvik.....erilrE
 +e+ ++lG GaF++V la +k tg+l+A+K+i+++ +++++ +i++E
 68730 23 FEFKETLGTGAFSEVVLAEEKATGKLFVAVKCIpkkalkgkeSSIENE 69
 ↑ ↑
 ikiLkk.dHPNIVkLydvfed.dklylVmEyceGdlGdLfdllkkrgrg
 i++L+k +H+NIV L d++e++++lylVm +++G G+Lfd++++g
 68730 70 IAVLRKiKHENIVALEDIYESpNHLYLVMQLVSG--GELFDRIIVEKGF-- 115
 ↑ ↑
 lrkvlse.earfyfrQilsaLeYLHsqgIiHRDLKPeNiLLds.....hv
 ++E++a ++rQ+l+a+ YLH++gI+HRDLKPeN+L s+++++ +
 68730 116 ----YTEkDASTLIROVLDAVYYLHRMGIVHRDLKPENLLYYSqdeesKI 161
 ↑ ↑ ↑ ↑
 KladFGlArql.....ttfvGTpeYmAPEvl...gYgkpavDiWSlGci
 +++DFGl++ +++++ +t +GTP Y+APEvl +++Y+k avD WS+G+i
 68730 162 MISDFGLSKMEgkgdvmSTACGTPGYVAPEVLaqkPYSK-AVDCWSIGVI 210
 lyElltGkpPFp..qldlifkkig.....SpeakdLikkll
 y+ll+G+pPF+++++ ++f++i++ +++ ++++++ S++akd+i++l+
 68730 211 AYILLCGYPPFYdeNDSKLFEQILkaeyefdsipywddiSDSAKDFIRNLM 260
 vkdPekRlta.eaLedeldikaHPff<-*
 +kdP+kR+t++++a + HP++
 68730 261 EKDPNKRYTCeQAAR-----HPWI 279

FIGURE 3B

tyrkin_6: domain 1 of 1, from 23 to 279: score 35.7, E = 4e-14
*->ltlgkklGeGaFGeVykGtlk...ieVAVKtLkeda....keeFlrE
+++++LG GaF eV++++ k ++ AVK++ + a +++++ + +E
68730 23 FEFKETLGTGAFSEVVLAEKAtgKLFVAVKCIPKKAlkgkESSIENE 69
↑ ↑
akiMkklGgkHpNiVklLlGvcteeegrrFmevePlmivmEymegGdLldyL
+ +++k+ kH+NiV+L + ++ l++vm +++gG L d++
68730 70 IAVLRKI--KHENIVALEDIYESP-----NHLYLVMQLVSGGELFDRI 110
↑
rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
++ + +d Q+ + YL+++++vHRDL N L+ ++ +++
68730 111 -VEKGfYTEKDASTLIROVLDAVYYLHRMGIVHRDLKPENLLYYSQDees 159
↑ ↑ ↑ ↑ ↑
vvKIsDFGLsRdlyddDkkGeskdYrkkggkggkgtllPirWmAPESlkd
+ IsDFGLs+ + + d+ +++ g+ + APE+l
68730 160 KIMISDFGLSKMEGKG-----DVMSTAC--GTPG-----YVAPEVLAQ 195
gkFtskSDVWSFGVlLWEiftlGeqPYpgeiqqfmsneevleylkkGyRl
+ ++ + D WS GV + i+ G +P ++ +++ ++e++ k ++
68730 196 KPYSKAVDCWSIGVIAIY-ILLCGYPPFYD-----ENDSKLFEQILKAEYE 239
pkPendlpisS....vtCPdelydlMlqCwaedPedRPtFsel..verl<
++ ++ + + d + +lM++ dP++R t ++ ++ +
68730 240 FDSPY-----WddisDSAKDFIRNLMEK----DPNKRYTCEQAarHPWI 279

FIGURE 3C

pkinese: domain 1 of 1, from 356 to 613: score 350.2, E = 2.3e-101
 *-->yelleklGeGsfgkVykakhk.tgkivAvKilkkels.....lrE
 ye++++G G+f++V++++h++t + +A+Ki++k++l++++ +E
 69112 356 YETGRVIGDGNFAVVKECRHReTRQAYAMKIIDKSRLKgkedmvdSE 402

 iqilkrIsHpNIvrlIlgvfedtdhhlylvmEymegGdLfdylrrngplse
 i i ++lsHpNIv+l++v+e td ++yl++Ey+ gGdLfd + + +++e
 69112 403 ILIIQSLSHPNIVKLHEVYE-TDMEIYLILEYVQGGDLFDAIIESVKFPE 451

 keakkialQilrGleYlHsngivHRDLKpeNILlden....gtvKiaDFG
 ++a ++ +++++l ++H+++ivHRDLKpeN+L+ +n++++ t+K+aDFG
 69112 452 PDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNedksTTLKLADFG 501
 ↑ ↑
 LArlI.eklttfvGTPwYmmAPEvilegrgysskvDvWSlGviLyElltg
 LA+ + + t++GTP+Y+ APE+ l+ +gy+ +vD+W+ GviLy ll+g
 69112 502 LAKHVvRPIFTVCGTPTYV-APEI-LSEKGYGLEVDMWAAGVILYILLCG 549

 gplfpgadlpaftggdevdqliifvklPfsdelpktridpleelfrikk
 +Pf+ ++ +elf+i++
 69112 550 -----FPPFRS-----PERDQDELFNIIQ 568

 r.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<-
 ++ + ++p ++n+S+++kdL++++L +DP+kR+ ta+++l+hpw+
 69112 569 LghfefLPPYWDNISDAAKDLVSRLLVVDPKKRY---TAHQVLQHPWI 613

*

FIGURE 4A

serkin_6: domain 1 of 1, from 356 to 613: score 372.7, E = 3.8e-108

*->YellkklGkGaFGkVylardkktgrlvAiKvik.....erilrE
 Ye ++++G G F++V+ +r+++t + +A+K+i++++ ++++++ +E
 69112 356 YETGRVIGDGNFAVVKECRHRETRQAYAMKIIDksrlkgkeDMVDSE 402

ikiLkk.dHPNIVkLydvfed.dklylVmEyceGdlGdLfdllkkrgrrg
 i i ++ HPNIVkL++v++e++ ++yl++Ey+ G GdLfd + + +
 69112 403 ILIIQSLSHPNIVKLHEVYETdMEIYLILEYVQG--GDLFDAIESVK-- 448

lrkvlsE.earfyfrQilsaLeYLHsqgIiHRDLKPeNiLLds.....h
 ++E++a+ ++ +++aL ++H++ I+HRDLKPeN+L+ +++++++
 69112 449 ----FPEpDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRnedkstT 494

vKlaDFGlaArql....ttfvGTpeYmAPEvl...gYgkpavDiWSlGcil
 +KlaDFGla+++ ++ t++GTP Y+APE+l+++gYg +vD+W+ G+il
 69112 495 LKLADFGlAKHVvrpiFTVCGTPTYVAPEILsekGYGL-EVDMWAAGVIL 543

yElltGkpPFp....qldlifkkig.....SpeakdLikkl
 y+ll+G pPF++++++d++f++i ++ + ++++++ S+ akdL+++l
 69112 544 YILLCGFPFRsperDQDELFNIIQlghfelfppywdniSDAAKDLVSRL 593

LvkdPekRlta.eaLedeldikaHPff<-*
 Lv+dP+kR+ta+++L+ HP++
 69112 594 LVVDPKKRYTAhQVLQ-----HPWI 613

FIGURE 4B

tyrkin_6: domain 1 of 1, from 356 to 613: score 50.0, E = 5.3e-15

*->ltlgkklGeGaFGeVykGtlk...ieVAVKtLkeda....keeFlrE
 + g+++G G+F +V +++ +++++ A K + ++ +++++ + +E

69112 356 YETGRVIGDGNFAVVKECRHRetrQAYAMKIIDKSRLkgkEDMVDSE 402

akiMkklGgkHpNiVklLlGvcteeegrrFmevePlmivmEymegGdLldyL
 + i +l +HpNiVkl+ v ++ +++++Ey+ gGdL d +

69112 403 ILIIQSL--SHPNIVKLHEVYETD-----MEIYLILEYVQGGLFDAI 443

rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
 ++ + ++ +d + + +k + ++k +vHRDL N Lv +n +++

69112 444 IESVK-FPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEdks 492

.vvKIsDFGLsRdlyddDkkGeskdYrkkggkggktllPirWmAPESlk
 ++ K +DFGL++ + ++ +g APE l

69112 493 tTLKLADFGLAKHVVRP-----IFTV----CGTP----TYVAPEILS 526

dgkFtskSDVWSFGVlLWEiftlGeqPYpgeiqqfmsneevleylkkGyR
 ++ + + D W+ GV L+ i+ G +P ++ + +e+++ ++ G+

69112 527 EKGYLEVDMWAAGVILY-ILLCGFPPFRSPE---RDQDELFNIIQLGHF 572

lpkPendlpiSsvtCPdelydlMlqCwaedPedRPtFsel..verl<-*
 P++ +d+ dl ++ dP++R t ++ ++ +

69112 573 EFLPPY-----WDNISDAAKDLVSRLLVDPKKRYTAHQVlqHPWI 613

FIGURE 4C